

Genetic And Phenotypic Responses To Selection For Dairy Traits In A Single Herd

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Introduction

Breeding values based on BLUP methodology have been available on dairy animals for over 20 years in many countries, for a large number of traits. Use of these breeding values in a selection programme should lead to changes in the genetic make-up of populations. Demonstrations of response to selection in experimental populations are well known and the change in traits, such as milk yield, over time has also been widely reported. Genetic correlations at national level are also well documented. In this study the result of using one selection goal in a single herd over a long period of time is reported for dairy traits. This includes both phenotypic changes in the selection criterion trait and also correlated responses in a range of other traits of significance to dairy production.

Material and methods

Background. The herd used in this study was the Langhill Herd now maintained by the Scottish Agricultural College at its Crichton Royal Farm, Dumfries, UK. The establishment of the herd has been described previously by Veerkamp *et al.* (1995) and recent management practices can be found in Pollott and Coffey (2008). The 200-cow herd was divided into a selection line (SL) and control line (CL). Selection in SL was based on bulls of the highest available fat+protein PTA in any one year but taking due regard of inbreeding. In CL, bulls were selected for having average UK genetic merit at the time of selection, based on the £PIN index (production only) used in the UK. The two genetic lines were also split into two feeding systems, a high-forage system (HF) and a high-concentrate system (HC).

Data used The genetic data used in this study comprised of PTAs derived from the UK national evaluations carried out in September 2009 for cows born between 1980 and 2006. The phenotypic data was derived from heifer records extracted from the SAC Langhill research database. In all, 42 production and type traits were available for analysis but only the key traits are reported here; these comprise milk, fertility, body measurements and health traits.

Statistical analyses Trends in PTAs were analysed by fitting year of birth, genetic line and feeding system to the PTA data. Non-linear trends were explored for each trait by fitting year of birth as a second-order polynomial. All analyses were carried out using the PROC GLM in SAS (SAS, 2006).

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Results and discussion

Data were available from 666 SL and 529 CL cows born between 1980 and 2006. The mean 305d fat+protein PTA by year of birth for each genetic line is shown in Figure 1.

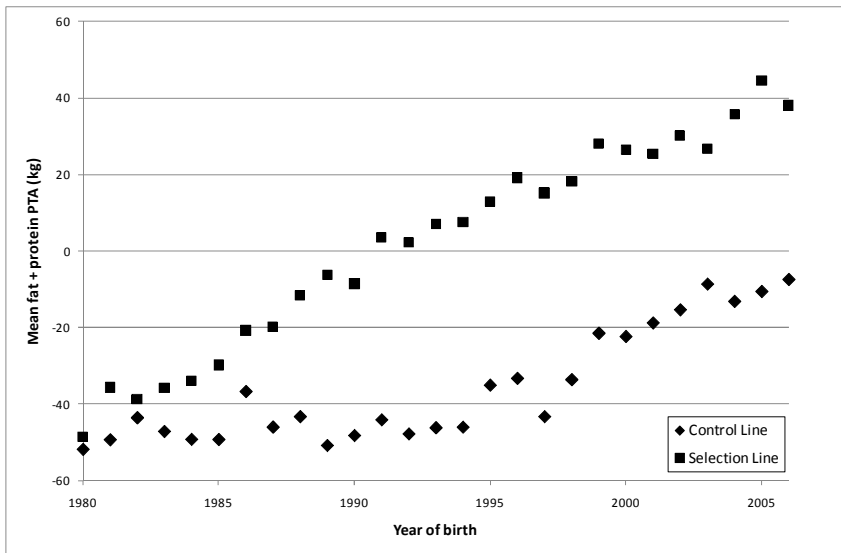


Figure 1: Trends in 305d fat + protein PTA for Selection and Control lines between 1980 and 2006 (kg/305d lactation)

SL cows showed an increase in 305d fat+protein PTA of $3.32 \pm 0.068 \text{ kg/y}$. The CL cows fat+protein PTA annual means showed little change between 1980 and 1994 but in later years there was an increase of $3.39 \pm 0.174 \text{ kg/y}$. The SL results demonstrate the efficacy of genetic selection at individual farm level using publicly available breeding information. Consistency of breeding objective results in genetic progress in a predictable and sustained manner. The CL results also demonstrate the power of selection. In this case the objective was to maintain the CL at the same genetic merit as the average UK dairy cow. Bulls used on the CL had £PIN values of around 0, the national average. The increase in fat+protein PTA from 1995 onwards reflects base changes in breeding value estimation which has happened every 5 years since 1995.

The result of fitting year of birth to the PTA of 16 traits is shown in Table 1. Year of birth was found to be a significant factor for all traits except persistency. The regressions for several traits were found to have a low R^2 value and demonstrated little change over the 26-year period. These included fat and protein percent, somatic cell count, lifespan and locomotion.

Substantial gains were made in the genetic merit of milk yield traits and the indexes commonly used in the UK. However a marked decline in fertility PTAs were found. This is explored further in Figure 2 where a curve was fitted to the calving interval PTA data; this

curve improved the residual mean square compared to the linear trend ($P < 0.05$). There is evidence that fertility PTA declined in the early years of this study but this decline has now stopped. Similar trends in the other fertility traits were observed (Not shown). Given that the selection criterion of this herd is for production only, this halt in fertility decline can only be ascribed to breeding decisions made by the breeding companies supplying the semen used in this herd who may already be selecting for bulls carrying better fertility genes.

Table 1. The results from fitting a linear regression on year of birth to the PTA of 16 traits from the Selection Line

Traits	R ²	Linear trend	s.e.	Regression model
<i>Selection criteria</i>				
305-d fat plus protein (kg)	0.78	3.32	0.0685	***
305-d milk yield (kg)	0.69	48.1	1.24	***
Pedigree index (£/lact.)	0.78	2.94	0.061	***
Profitable life ind. (£/life)	0.76	10.7	0.24	***
<i>Other milk traits</i>				
Fat %	0.05	-0.00335	0.0006	***
Protein %	0.09	0.00224	0.0003	***
Persistency (%)	0.01	0.0127	0.0069	NS
Milk yield on d 110 (kg)	0.67	0.273	0.0088	***
<i>Fertility</i>				
Calving interval (d)	0.49	0.661	0.0310	***
Day of 1 st service	0.48	0.385	0.0182	***
56-day non-return rate	0.42	-0.00340	0.0002	***
No. of ins. per conception	0.37	0.00694	0.0004	***
<i>Health</i>				
Somatic cell count (%)	0.06	0.287	0.0492	***
Lifespan (y)	0.07	0.00564	0.0008	***
Condition score (0-5)	0.42	-0.0488	0.0026	***
Locomotion (1-9)	0.07	0.0250	0.0037	***

The phenotypic trends in 305d milk yield are shown in Figure 3, with separate trends for the two genetic lines and two feeding systems. The SL cows maintained on the high concentrate diet increased their 305d milk yield by 128kg/y whilst those on the high forage diet gained 25kg/y. Both CL groups lost milk yield initially but after 1990 started to increase their milk yield, with the HC group making faster gains in the latter years than the HC-SL group.

Conclusion

This work has demonstrated the gains that can be made by a single producer using the readily available information on performance trait PTA. A phenotypic increase in 305d milk yield of 4,000kg from a base of 6000kg is impressive. This work also demonstrates the gains that can be made from the same genetics (SL) but fed in two different ways. The results of this herd also reflect the trends found at national level where a decline in fertility over recent years can be halted using appropriate selection measures.

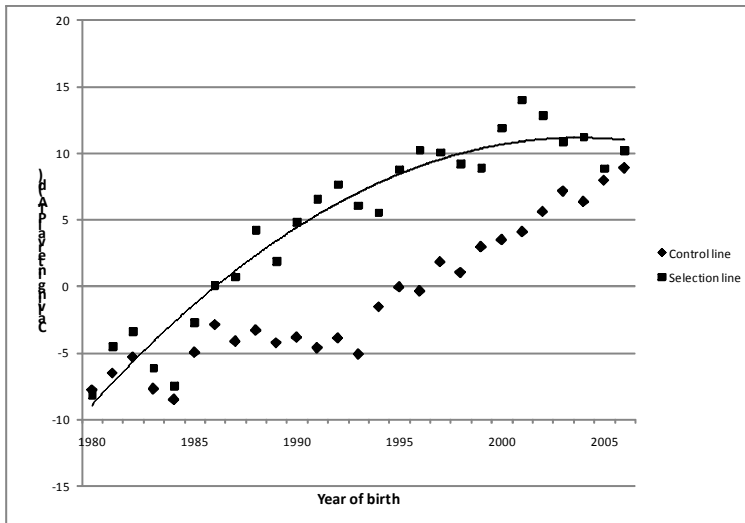


Figure 2. The Selection and Control Line time trends in calving interval PTA (d)

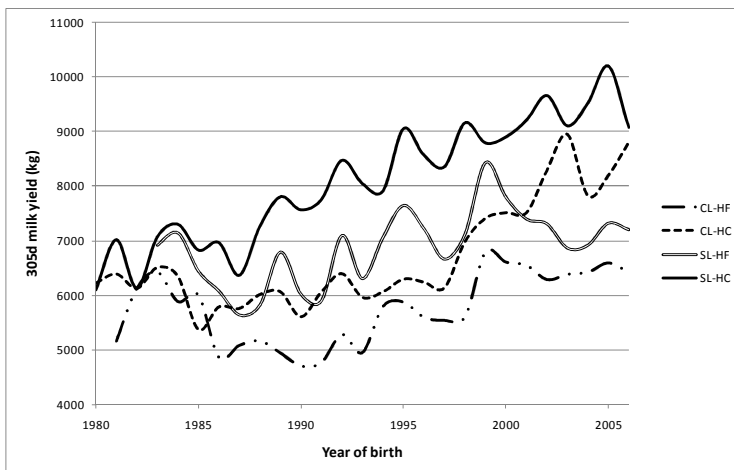


Figure 3. The trends in phenotypic performance for 305d milk yield for the four genetic line by feeding system groups

References

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